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RAW SEQUENCE LISTING   DATE: 07/18/2001
PATENT APPLICATION: **US/09/596,101A** TIME: 09:29:30

Input Set : **A:\PTO_VSK.txt**
Output Set: **N:\CRF3\07182001\I596101A.raw**

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 3 <110> APPLICANT: VLAAMS INTERUNIVERSITAIR INSTITUUT VOOR BIOTECHNOL
 5 <120> TITLE OF INVENTION: Peptides and nucleic acids derived from Eisenia foetida and
the use
 6       thereof
 8 <130> FILE REFERENCE: 2676-4432US
10 <140> CURRENT APPLICATION NUMBER: US 09/596101A
11 <141> CURRENT FILING DATE: 2000-06-16
13 <150> PRIOR APPLICATION NUMBER: PCT/EP98/08169
14 <151> PRIOR FILING DATE: 1998-12-16
16 <150> PRIOR APPLICATION NUMBER: 97203974.7
17 <151> PRIOR FILING DATE: 1997-12-17
19 <160> NUMBER OF SEQ ID NOS: 3
21 <170> SOFTWARE: PatentIn version 3.0
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 13
25 <212> TYPE: PRT
26 <213> ORGANISM: Eisenia fetida
28 <400> SEQUENCE: 1
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31 1               5                   10
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34 <211> LENGTH: 1155
35 <212> TYPE: DNA
36 <213> ORGANISM: Eisenia fetida
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39 <221> NAME/KEY: CDS
40 <222> LOCATION: (1)..(1152)
42 <220> FEATURE:
43 <221> NAME/KEY: sig_peptide
44 <222> LOCATION: (1)..(51)
46 <220> FEATURE:
47 <221> NAME/KEY: mat_peptide
48 <222> LOCATION: (52)..()
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52 Met Arg Trp Thr Leu Val Val Leu Cys Leu Leu Phe Gly Glu Gly Phe
53          -15                 -10                 -5
55 gcc ttc acc gac tgg gat caa tat cac atc gtc tgg cag gac gaa ttc      96
56 Ala Phe Thr Asp Trp Asp Gln Tyr His Ile Val Trp Gln Asp Glu Phe
57 -1 1             5                   10                  15
59 gat tac ttt gat ggc gcg aag tgg caa cat gag gtc aca gca act ggc     144
60 Asp Tyr Phe Asp Gly Ala Lys Trp Gln His Glu Val Thr Ala Thr Gly
61                 20                  25                  30
63 gga ggg aac agc gaa ttc caa ctg tac aca cag gat ggg gcc aac agc     192
64 Gly Gly Asn Ser Glu Phe Gln Leu Tyr Thr Gln Asp Gly Ala Asn Ser
65                 35                  40                  45
67 ttc gtt cga gat gga aag ctt ttc att aag ccg acg ttg ctg gct gac     240
68 Phe Val Arg Asp Gly Lys Leu Phe Ile Lys Pro Thr Leu Leu Ala Asp
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71 aac atc aac cca cag acg ggt gcg cca ttt gga acc gat ttc atg tac      288
72 Asn Ile Asn Pro Gln Thr Gly Ala Pro Phe Gly Thr Asp Phe Met Tyr
73     65                    70                    75
75 aat gga gtt cta gat gtc tgg gct atg tac ggg gcc tgc acg aat acg      336
76 Asn Gly Val Leu Asp Val Trp Ala Met Tyr Gly Ala Cys Thr Asn Thr
77 80                    85                    90                    95
79 gac aac aac gga tgc tac agg acg gga gcc gct ggc gac att cca ccg      384
80 Asp Asn Asn Gly Cys Tyr Arg Thr Gly Ala Ala Gly Asp Ile Pro Pro
81                 100                   105                   110
83 gcc atg tcg gca cga gtt cga acc ttc cag aaa tac agc ttc acc cac      432
84 Ala Met Ser Ala Arg Val Arg Thr Phe Gln Lys Tyr Ser Phe Thr His
85             115                   120                   125
87 gga cgc gtt gtc gtt cac gcc aag atg ccc gtc gga gac tgg ctc tgg      480
88 Gly Arg Val Val Val His Ala Lys Met Pro Val Gly Asp Trp Leu Trp
89         130                   135                   140
91 cca gcc att tgg atg ttg ccg gag gat tgg gtc tat ggc gga tgg cct      528
92 Pro Ala Ile Trp Met Leu Pro Glu Asp Trp Val Tyr Gly Gly Trp Pro
93     145                   150                   155
95 cga tcg ggc gag atc gac atc att gaa aca atc ggc aac cga gat ttc      576
96 Arg Ser Gly Glu Ile Asp Ile Ile Glu Thr Ile Gly Asn Arg Asp Phe
97 160                   165                   170                   175
99 aag aac act ggt gga gag ttc ctt gga att cag aag atg gga tca acg      624
100 Lys Asn Thr Gly Gly Glu Phe Leu Gly Ile Gln Lys Met Gly Ser Thr
101                 180                   185                   190
103 atg cac tgg ggt cca gga tgg gac gac aac cga tac tgg ctg acc agc      672
104 Met His Trp Gly Pro Gly Trp Asp Asp Asn Arg Tyr Trp Leu Thr Ser
105             195                   200                   205
107 ctt ccg aaa cac tca gac gat tgg aac tac ggt gac aac ttc cac acg      720
108 Leu Pro Lys His Ser Asp Asp Trp Asn Tyr Gly Asp Asn Phe His Thr
109         210                   215                   220
111 ttc tgg ttc gac tgg agt ccc aac gga ctg agg ttc ttc gta gac gac      768
112 Phe Trp Phe Asp Trp Ser Pro Asn Gly Leu Arg Phe Phe Val Asp Asp
113     225                   230                   235
115 gag aac cag gct ctg ctc gat gtt cct tat cct ctg att gat gcg aat      816
116 Glu Asn Gln Ala Leu Leu Asp Val Pro Tyr Pro Leu Ile Asp Ala Asn
117 240                   245                   250                   255
119 cca tgg tgg gtg gat ttc tgg gag tgg gga aag ccc tgg ctt cct caa      864
120 Pro Trp Trp Val Asp Phe Trp Glu Trp Gly Lys Pro Trp Leu Pro Gln
121                 260                   265                   270
123 tac gaa aat gac aat cca tgg gct gga gga acg aac ctg gct ccc ttc      912
124 Tyr Glu Asn Asp Asn Pro Trp Ala Gly Gly Thr Asn Leu Ala Pro Phe
125             275                   280                   285
127 gac caa aat ttc cac ttc att ctg aac gtg gct gtc gga gga acg aac      960
128 Asp Gln Asn Phe His Phe Ile Leu Asn Val Ala Val Gly Gly Thr Asn
129         290                   295                   300
131 ggc ttc atc ccg gac ggt tgc atc aat cgc ggc gga gac ccg gcc ctg     1008
132 Gly Phe Ile Pro Asp Gly Cys Ile Asn Arg Gly Gly Asp Pro Ala Leu
133     305                   310                   315
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135 cag aag ccg tgg agc aat ggg gac tgg tac aac gat gca atg agg aaa      1056
136 Gln Lys Pro Trp Ser Asn Gly Asp Trp Tyr Asn Asp Ala Met Arg Lys
137 320             325             330             335
139 ttc ttc gac gcc aga gga aac tgg aag tgg acg tgg gat gac gag gga      1104
140 Phe Phe Asp Ala Arg Gly Asn Trp Lys Trp Thr Trp Asp Asp Glu Gly
141             340             345             350
143 gac aac aat gcc atg cag gtc gat tac atc cga gtc tac aag cgc aac      1152
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145             355             360             365
147 tga                                                             1155
150 <210> SEQ ID NO: 3
151 <211> LENGTH: 384
152 <212> TYPE: PRT
153 <213> ORGANISM: Eisenia fetida
155 <400> SEQUENCE: 3
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161 Ala Phe Thr Asp Trp Asp Gln Tyr His Ile Val Trp Gln Asp Glu Phe
162 -1  1           5               10                  15
165 Asp Tyr Phe Asp Gly Ala Lys Trp Gln His Glu Val Thr Ala Thr Gly
166             20              25              30
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170             35              40              45
173 Phe Val Arg Asp Gly Lys Leu Phe Ile Lys Pro Thr Leu Leu Ala Asp
174         50              55              60
177 Asn Ile Asn Pro Gln Thr Gly Ala Pro Phe Gly Thr Asp Phe Met Tyr
178     65              70              75
181 Asn Gly Val Leu Asp Val Trp Ala Met Tyr Gly Ala Cys Thr Asn Thr
182 80              85              90                  95
185 Asp Asn Asn Gly Cys Tyr Arg Thr Gly Ala Ala Gly Asp Ile Pro Pro
186             100             105             110
189 Ala Met Ser Ala Arg Val Arg Thr Phe Gln Lys Tyr Ser Phe Thr His
190             115             120             125
193 Gly Arg Val Val Val His Ala Lys Met Pro Val Gly Asp Trp Leu Trp
194         130             135             140
197 Pro Ala Ile Trp Met Leu Pro Glu Asp Trp Val Tyr Gly Gly Trp Pro
198     145             150             155
201 Arg Ser Gly Glu Ile Asp Ile Ile Glu Thr Ile Gly Asn Arg Asp Phe
202 160             165             170                 175
205 Lys Asn Thr Gly Gly Glu Phe Leu Gly Ile Gln Lys Met Gly Ser Thr
206             180             185             190
209 Met His Trp Gly Pro Gly Trp Asp Asp Asn Arg Tyr Trp Leu Thr Ser
210             195             200             205
213 Leu Pro Lys His Ser Asp Asp Trp Asn Tyr Gly Asp Asn Phe His Thr
214         210             215             220
217 Phe Trp Phe Asp Trp Ser Pro Asn Gly Leu Arg Phe Phe Val Asp Asp
218     225             230             235
221 Glu Asn Gln Ala Leu Leu Asp Val Pro Tyr Pro Leu Ile Asp Ala Asn
222 240             245             250             255
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225 Pro Trp Trp Val Asp Phe Trp Glu Trp Gly Lys Pro Trp Leu Pro Gln
226             260             265             270
229 Tyr Glu Asn Asp Asn Pro Trp Ala Gly Gly Thr Asn Leu Ala Pro Phe
230             275             280             285
233 Asp Gln Asn Phe His Phe Ile Leu Asn Val Ala Val Gly Gly Thr Asn
234         290             295             300
237 Gly Phe Ile Pro Asp Gly Cys Ile Asn Arg Gly Gly Asp Pro Ala Leu
238     305             310             315
241 Gln Lys Pro Trp Ser Asn Gly Asp Trp Tyr Asn Asp Ala Met Arg Lys
242 320             325             330             335
245 Phe Phe Asp Ala Arg Gly Asn Trp Lys Trp Thr Trp Asp Asp Glu Gly
246             340             345             350
249 Asp Asn Asn Ala Met Gln Val Asp Tyr Ile Arg Val Tyr Lys Arg Asn
250         355             360             365
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VERIFICATION SUMMARY . . -   DATE: 07/18/2001
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